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SEQUENCE LISTING

<110> Kharbanda, Surrender
Kufe, Donald

<120> Modulation of Interaction of MUC1 with MUC1 Ligands

<130> ILEX:094WO

<140> Unknown

<141> 2004-10-21

<150> 60/514,198

<151> 2003-10-24

<150> 60/519,822

<151> 2003-11-12

<160> 71

<170> PatentIn version 3.3

<210> 1

<211> 164

<212> PRT

<213> Homo sapiens

<400> 1

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
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Val Leu Thr Ala Thr Thr Ala Pro Lys Pro Ala Thr Val Val Thr Gly
20 25 30

Ser Gly His Ala Ser Ser Thr Pro Gly Gly Glu Lys Glu Thr Ser Ala
35 40 45

Thr Gln Arg Ser Ser Val Pro Ser Ser Thr Glu Lys Asn Ala Phe Asn
50 55 60

Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg
65 70 75 80

Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu
85 90 95

Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu
100 105 110

Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Met Glu Thr
115 120 125

Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr
 130 135 140

Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln
 145 150 155 160

Ser Gly Ala Gly

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 <213> Homo sapiens

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 aatgctttta attcctctct ggaagatccc agcaccgact actaccaaga gctgcagaga 240
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 <212> PRT
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<400> 3

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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35 40 45

Thr Glu Lys Asn Ala Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp
 50 55 60

Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile

Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35 40 45

Thr Glu Lys Asn Ala Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser
 50 55 60

Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser
 65 70 75 80

Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu
 85 90 95

Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe
 100 105 110

Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly
 115 120 125

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
 130 135 140

Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
 145 150 155 160

Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
 165 170

<210> 6
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<210> 7
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<400> 7

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Thr
 35 40 45

Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln
 50 55 60

Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg
 65 70 75 80

Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr
 85 90 95

Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu
 100 105 110

Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp
 115 120 125

Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
 130 135 140

<210> 8
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 cagagaagtt cagtgccag caccgactac taccaagagc tgcagagaga catttctgaa 180
 atgtttttgc agatttataa acaagggggt tttctgggcc tctccaatat taagttcagg 240
 ccaggatctg tggtggtaca attgactctg gccttccgag aaggtaccat caatgtccac 300
 gacatggaga cacagttcaa tcagtataaa acggaagcag cctctcgata taacctgacg 360

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 <212> PRT
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Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35 40 45

Thr Glu Lys Asn Ala Ile Pro Ala Pro Thr Thr Thr Lys Ser Cys Arg
 50 55 60

Glu Thr Phe Leu Lys Trp Pro Gly Ser Val Val Val Gln Leu Thr Leu
 65 70 75 80

Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe
 85 90 95

Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser
 100 105 110

Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly
 115 120 125

Ala Gly
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<210> 10
 <211> 390
 <212> DNA
 <213> Homo sapiens

<400> 10

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 cagagaagtt cagtgccag ctctactgag aagaatgcta tcccagcacc gactactacc 180
 aagagctgca gagagacatt tctgaaatgg ccaggatctg tgggtgtaca attgactctg 240
 gccttccgag aaggtaccat caatgtccac gacatggaga cacagttcaa tcagtataaa 300

acggaagcag cctctcgata taacctgacg atctcagacg tcagcgtgag tgatgtgcca 360
 tttcctttct ctgcccagtc tggggctggg 390

<210> 11
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 11

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 1 5 10 15

Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly Gly
 20 25 30

Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val Val
 35 40 45

Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp Val
 50 55 60

Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn
 65 70 75 80

Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser
 85 90 95

Ala Gln Ser Gly Ala Gly
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<210> 12
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 <213> Homo sapiens

<400> 12

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 gctggg 306

<210> 13

<211> 375
 <212> PRT
 <213> Homo sapiens

<400> 13

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35 40 45

Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
 50 55 60

Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
 65 70 75 80

Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
 85 90 95

Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
 100 105 110

Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Pro Ala Pro
 115 120 125

Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser Ala Pro Asp Thr
 130 135 140

Arg Pro Ala Pro Gly Ser Thr Ala Pro Pro Ala His Gly Val Thr Ser
 145 150 155 160

Ala Pro Asp Asn Arg Pro Ala Leu Gly Ser Thr Ala Pro Pro Val His
 165 170 175

Asn Val Thr Ser Ala Ser Gly Ser Ala Ser Gly Ser Ala Ser Thr Leu
 180 185 190

Val His Asn Gly Thr Ser Ala Arg Ala Thr Thr Thr Pro Ala Ser Lys
 195 200 205

Ser Thr Pro Phe Ser Ile Pro Ser His His Ser Asp Thr Pro Thr Thr
 210 215 220

Leu Ala Ser His Ser Thr Lys Thr Asp Ala Ser Ser Thr His His Ser
225 230 235 240

Thr Val Pro Pro Leu Thr Ser Ser Asn His Ser Thr Ser Pro Gln Leu
245 250 255

Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn Leu
260 265 270

Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln Glu
275 280 285

Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln Gly
290 295 300

Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val Val
305 310 315 320

Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His Asp
325 330 335

Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr
340 345 350

Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro Phe
355 360 365

Ser Ala Gln Ser Gly Ala Gly
370 375

<210> 14
<211> 1125
<212> DNA
<213> Homo sapiens

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cagagaagtt cagtgccag ctctactgag aagaatgctg tgagtatgac cagcagcgta 180
ctctccagcc acagccccgg ttcaggctcc tccaccactc agggacagga tgtcactctg 240
gccccggcca cggaaccagc ttcagggttca gctgccacct ggggacagga tgtcacctcg 300
gtcccagtca ccaggccagc cctgggctcc accaccccg cagcccacga tgtcacctca 360
gccccggaca acaagccagc cccgggctcc accgcccccc cagcccacgg tgtcacctcg 420

gccccggaca ccaggccggc cccgggctcc accgcccccc cagcccatgg tgtcacctcg 480
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 tataaacaag ggggttttct gggcctctcc aatattaagt tcaggccagg atctgtggtg 960
 gtacaattga ctctggcctt ccgagaaggt accatcaatg tccacgacgt ggagacacag 1020
 ttcaatcagt ataaaacgga agcagcctct cgatataacc tgacgatctc agacgtcagc 1080
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<210> 15
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 <212> PRT
 <213> Homo sapiens

<400> 15

Met Thr Pro Gly Thr Gln Ser Pro Phe Phe Leu Leu Leu Leu Leu Thr
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Val Leu Thr Val Val Thr Gly Ser Gly His Ala Ser Ser Thr Pro Gly
 20 25 30

Gly Glu Lys Glu Thr Ser Ala Thr Gln Arg Ser Ser Val Pro Ser Ser
 35 40 45

Thr Glu Lys Asn Ala Val Ser Met Thr Ser Ser Val Leu Ser Ser His
 50 55 60

Ser Pro Gly Ser Gly Ser Ser Thr Thr Gln Gly Gln Asp Val Thr Leu
 65 70 75 80

Ala Pro Ala Thr Glu Pro Ala Ser Gly Ser Ala Ala Thr Trp Gly Gln
 85 90 95

Asp Val Thr Ser Val Pro Val Thr Arg Pro Ala Leu Gly Ser Thr Thr
 100 105 110

Pro Pro Ala His Asp Val Thr Ser Ala Pro Asp Asn Lys Asn Arg Pro

115	120	125
Ala Leu Gly Ser Thr Ala	Pro Pro Val His Asn	Val Thr Ser Ala Ser
130	135	140
Gly Ser Ala Ser Gly Ser	Ala Ser Thr Leu Val	His Asn Gly Thr Ser
145	150	155
Ala Arg Ala Thr Thr Thr	Pro Ala Ser Lys Ser Thr	Pro Phe Ser Ile
165	170	175
Pro Ser His His Ser Asp	Thr Pro Thr Thr Leu Ala	Ser His Ser Thr
180	185	190
Lys Thr Asp Ala Ser Ser	Thr His His Ser Thr Val	Pro Pro Leu Thr
195	200	205
Ser Ser Asn His Ser Thr	Ser Pro Gln Leu Ser Thr	Gly Val Ser Phe
210	215	220
Phe Phe Leu Ser Phe His	Ile Ser Asn Leu Gln Phe	Asn Ser Ser Leu
225	230	235
Glu Asp Pro Ser Thr Asp	Tyr Tyr Gln Glu Leu Gln	Arg Asp Ile Ser
245	250	255
Glu Met Phe Leu Gln Ile	Tyr Lys Gln Gly Gly Phe	Leu Gly Leu Ser
260	265	270
Asn Ile Lys Phe Arg Pro	Gly Ser Val Val Val Gln	Leu Thr Leu Ala
275	280	285
Phe Arg Glu Gly Thr Ile	Asn Val His Asp Val Glu	Thr Gln Phe Asn
290	295	300
Gln Tyr Lys Thr Glu Ala	Ala Ser Arg Tyr Asn Leu	Thr Ile Ser Asp
305	310	315
Val Ser Val Ser Asp Val	Pro Phe Pro Phe Ser Ala	Gln Ser Gly Ala
325	330	335

Gly

<210> 16
 <211> 1011

<212> DNA

<213> Homo sapiens

<400> 16

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cagagaagtt cagtgccagc ctctactgag aagaatgctg tgagtatgac cagcagcgta      180
ctctccagcc acagccccgg ttcaggctcc tccaccactc agggacagga tgtcactctg      240
gccccggcca cggaaccagc ttcagggttca gctgccacct ggggacagga tgtcacctcg      300
gtcccagtca ccaggccagc cctgggctcc accaccccg cagcccacga tgtcacctca      360
gccccggaca acaagaacag gccgccttg ggctccaccg cccctccagt ccacaatgtc      420
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gccaggggcta ccacaacccc agccagcaag agcactccat tctcaattcc cagccaccac      540
tctgatactc ctaccaccct tgccagccat agcaccaaga ctgatgccag tagcactcac      600
catagcacgg tacctcctct cacctcctcc aatcacagca cttctcccca gttgtctact      660
ggggtctctt tctttttcct gtcttttcac atttcaaacc tccagtttaa ttcctctctg      720
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gtggtggtac aattgactct ggccttcga gaaggtacca tcaatgtcca cgacgtggag      900
acacagttca atcagtataa aacggaagca gcctctcgat ataacctgac gatctcagac      960
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<210> 17

<211> 175

<212> PRT

<213> Homo sapiens

<400> 17

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Ala Thr Thr Thr Pro Ala Ser Lys Ser Thr Pro Phe Ser Ile Pro Ser
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His His Ser Asp Thr Pro Thr Thr Leu Ala Ser His Ser Thr Lys Thr
20           25           30

Asp Ala Ser Ser Thr His His Ser Thr Val Pro Pro Leu Thr Ser Ser
35           40           45

Asn His Ser Thr Ser Pro Gln Leu Ser Thr Gly Val Ser Phe Phe Phe
50           55           60

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Leu Ser Phe His Ile Ser Asn Leu Gln Phe Asn Ser Ser Leu Glu Asp
65 70 75 80

Pro Ser Thr Asp Tyr Tyr Gln Glu Leu Gln Arg Asp Ile Ser Glu Met
85 90 95

Phe Leu Gln Ile Tyr Lys Gln Gly Gly Phe Leu Gly Leu Ser Asn Ile
100 105 110

Lys Phe Arg Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg
115 120 125

Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr
130 135 140

Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser
145 150 155 160

Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
165 170 175

<210> 18
<211> 525
<212> DNA
<213> Homo sapiens

<400> 18
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acggtacctc ctctcacctc ctccaatcac agcacttctc cccagttgtc tactgggggc 180
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<210> 19
<211> 58
<212> PRT
<213> Homo sapiens

<400> 19

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Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala
20 25 30

Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro
35 40 45

Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly
50 55

<210> 20

<211> 174

<212> DNA

<213> Homo sapiens

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gacgtcagcg tgagtgatgt gccatttcct ttctctgccc agtctggggc tggg 174

<210> 21

<211> 50

<212> PRT

<213> Homo sapiens

<400> 21

Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn
1 5 10 15

Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala
20 25 30

Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro
35 40 45

Phe Pro
50

<210> 22

<211> 150

<212> DNA

<213> Homo sapiens

<400> 22

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gacgtcagcg tgagtgatgt gccatttcct

150

<210> 23

<211> 49

<212> PRT

<213> Homo sapiens

<400> 23

Phe Arg Glu Gly Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn
 1 5 10 15

Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp
 20 25 30

Val Ser Val Ser Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala
 35 40 45

Gly

<210> 24

<211> 147

<212> DNA

<213> Homo sapiens

<400> 24

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cctttctctg cccagtctgg ggctggg 147

<210> 25

<211> 120

<212> PRT

<213> Homo sapiens

<400> 25

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Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln
 20 25 30

Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln
 35 40 45

Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val
 50 55 60

Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His
65 70 75 80

Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg
85 90 95

Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro
100 105 110

Phe Ser Ala Gln Ser Gly Ala Gly
115 120

<210> 26
<211> 360
<212> DNA
<213> Homo sapiens

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atgtttttgc agatttataa acaaggggggt tttctgggcc tctccaatat taagttcagg 180
ccaggatctg tgggtggtaca attgactctg gccttccgag aaggtaccat caatgtccac 240
gacatggaga cacagttcaa tcagtataaa acggaagcag cctctcgata taacctgacg 300
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<210> 27
<211> 77
<212> PRT
<213> Homo sapiens

<400> 27

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20 25 30

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
35 40 45

Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
50 55 60

Asp Val Pro Phe Pro Phe Ser Ala Gln Ser Gly Ala Gly

65

70

75

<210> 28

<211> 231

<212> DNA

<213> Homo sapiens

<400> 28

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acacagttca atcagtataa aacggaagca gcctctcgat ataacctgac gatctcagac      180
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<210> 29

<211> 112

<212> PRT

<213> Homo sapiens

<400> 29

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Leu Ser Thr Gly Val Ser Phe Phe Phe Leu Ser Phe His Ile Ser Asn
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Leu Gln Phe Asn Ser Ser Leu Glu Asp Pro Ser Thr Asp Tyr Tyr Gln
          20           25           30

```

```

Glu Leu Gln Arg Asp Ile Ser Glu Met Phe Leu Gln Ile Tyr Lys Gln
          35           40           45

```

```

Gly Gly Phe Leu Gly Leu Ser Asn Ile Lys Phe Arg Pro Gly Ser Val
          50           55           60

```

```

Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly Thr Ile Asn Val His
65           70           75           80

```

```

Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg
          85           90           95

```

```

Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser Asp Val Pro Phe Pro
          100          105          110

```

<210> 30

<211> 336

<212> DNA

<213> Homo sapiens

<400> 30

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ctgtctactg gggctctctt ctttttcttg tcttttcaca tttcaaacct ccagtttaat      60

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tcctctctgg aagatcccag caccgactac taccaagagc tgcagagaga catttctgaa 120
 atgtttttgc agatttataa acaaggggggt tttctggggc tctccaatat taagtccagg 180
 ccaggatctg tgggtggtaca attgactctg gccttccgag aaggtaccat caatgtccac 240
 gacatggaga cacagttcaa tcagtataaa acggaagcag cctctcgata taacctgacg 300
 atctcagacg tcagcgtgag tgatgtgcca tttcct 336

<210> 31
 <211> 66
 <212> PRT
 <213> Homo sapiens

<400> 31

Ile Pro Ala Pro Thr Thr Thr Lys Ser Cys Arg Glu Thr Phe Leu Lys
 1 5 10 15

Trp Pro Gly Ser Val Val Val Gln Leu Thr Leu Ala Phe Arg Glu Gly
 20 25 30

Thr Ile Asn Val His Asp Val Glu Thr Gln Phe Asn Gln Tyr Lys Thr
 35 40 45

Glu Ala Ala Ser Arg Tyr Asn Leu Thr Ile Ser Asp Val Ser Val Ser
 50 55 60

Asp Val
 65

<210> 32
 <211> 198
 <212> DNA
 <213> Homo sapiens

<400> 32

atcccagcac cgactactac caagagctgc agagagacat ttctgaaatg gccaggatct 60
 gtggtggtac aattgactct ggccttccga gaaggtacca tcaatgtcca cgacatggag 120
 acacagttca atcagtataa aacggaagca gcctctcgat ataacctgac gatctcagac 180
 gtcagcgtga gtgatgtg 198

<210> 33
 <211> 232
 <212> PRT
 <213> HS

<400> 33

Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala

1	5	10	15
Pro Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro	20	25	30
Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val	35	40	45
Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val	50	55	60
Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln	65	70	75
Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln	85	90	95
Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala	100	105	110
Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro	115	120	125
Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr	130	135	140
Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser	145	150	155
Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr	165	170	175
Lys Thr Thr Pro Pro Val Leu Asp Ser Val Gly Ser Phe Phe Leu Tyr	180	185	190
Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe	195	200	205
Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys	210	215	220
Ser Leu Ser Leu Ser Pro Gly Lys	225	230	

<210> 34
<211> 699

<212> DNA

<213> HS

<400> 34

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gagcccaaatt cttgtgacaa aactcacaca tgcccaccgt gccagcacc tgaactcctg      60
gggggaccgt cagtcttctt cttcccccca aaaccaagg acaccctcat gatctcccgg      120
acccttgagg tcacatgctt ggtggtggac gtgagccacg aagaccctga ggtcaagtgc      180
aactggtacg tggacggcgt ggaggtgcat aatgccaaga caaagccgcg ggaggagcag      240
tacaacagca cgtaccgtgt ggtcagcgtc ctcaccgtcc tgcaccagga ctggctgaat      300
ggcaaggagt acaagtgcaa ggtctccaac aaagccctcc cagcccccat cgagaaaacc      360
atctccaaag ccaaagggca gccccgagaa ccacaggtgt acaccctgcc cccatcccgg      420
gatgagctga ccaagaacca ggtcagcctg acctgcctgg tcaaaggctt ctatccagc      480
gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct      540
cccgtgctgg actccgtcgg ctcttctctt ctctacagca agctcaccgt ggacaagagc      600
aggtggcagc aggggaacgt cttctcatgc tccgtgatgc atgaggctct gcacaaccac      660
tacacgcaga agagcctctc cctgtctccg ggtaaata      699

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<210> 35

<211> 230

<212> PRT

<213> HS

<400> 35

```

Lys Ser Cys Asp Lys Pro His Thr Cys Pro Leu Cys Pro Ala Pro Glu
1           5           10           15

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
          20           25           30

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
          35           40           45

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
          50           55           60

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
65           70           75           80

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
          85           90           95

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro

```

100	105	110
Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu		
115	120	125
Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn		
130	135	140
Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile		
145	150	155
		160
Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Ala		
165	170	175
Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys		
180	185	190
Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys		
195	200	205
Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu		
210	215	220
Ser Leu Ser Pro Gly Lys		
225	230	

<210> 36
 <211> 690
 <212> DNA
 <213> HS

<400> 36
 aaatcttgtag acaaacctca cacatgccca ctgtgccag cacctgaact cctgggggga 60
 ccgtcagttc tcctcttccc cccaaaaccc aaggacaccc tcatgatctc ccggaccct 120
 gaggtcacat gcgtgggtgg ggacgtgagc cacgaagacc ctgaggtcaa gttcaactgg 180
 tacgtggagc gcgtggaggt gcataatgcc aagacaaagc cgcgggagga gcagtacaac 240
 agcacgtacc gtgtggtcag cgtcctcacc gtctgcacc aggactggct gaatggcaag 300
 gactacaagt gcaaggtctc caacaaagcc ctcccagccc ccatcgagaa aacctctcc 360
 aaagccaaag ggcagccccg agaaccacag gtgtacaccc tgcccccatc ccgggatgag 420
 ctgaccaaga accaggtcag cctgacctgc ctagtcaaag gcttctatcc cagcgacatc 480
 gccgtggagt gggagagcaa tgggcagccg gagaacaact acaaggccac gcctcccggtg 540
 ctggactccg acggctcctt cttcctctac agcaagctca ccgtggacaa gagcaggtgg 600

cagcagggga acgtcttctc atgctccgtg atgcatgagg ctctgcacaa ccactacacg 660
 cagaagagcc tctccctgtc tccgggtaaa 690

<210> 37
 <211> 228
 <212> PRT
 <213> HS

<400> 37

Glu Arg Lys Cys Cys Val Glu Cys Pro Pro Cys Pro Ala Pro Pro Val
 1 5 10 15

Ala Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu
 20 25 30

Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser
 35 40 45

His Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Met Glu
 50 55 60

Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr
 65 70 75 80

Phe Arg Val Val Ser Val Leu Thr Val Val His Gln Asp Trp Leu Asn
 85 90 95

Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ala Pro
 100 105 110

Ile Glu Lys Thr Ile Ser Lys Thr Lys Gly Gln Pro Arg Glu Pro Gln
 115 120 125

Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val
 130 135 140

Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val
 145 150 155 160

Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro
 165 170 175

Pro Met Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr
 180 185 190

Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val

195

200

205

Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu
 210 215 220

Ser Pro Gly Lys
 225

<210> 38
 <211> 687
 <212> DNA
 <213> HS

<400> 38
 gagcgcaaat gttgtgtcga gtgcccaccg tgcccagcac cacctgtggc aggaccgtca 60
 gtcttctctt tcccccaaaa acccaaggac accctcatga tctcccggac ccctgaggtc 120
 acgtgcgtgg tgggtggacgt gagccacgaa gaccccgagg tccagttcaa ctggtacgtg 180
 gacggcatgg aggtgcataa tgccaagaca aagccacggg aggagcagtt caacagcacg 240
 ttccgtgtgg tcagcgtcct caccgtcgtg caccaggact ggctgaacgg caaggagtag 300
 aagtgcgaagg tctccaacaa aggcctccca gcccctatcg agaaaaccat ctccaaaacc 360
 aaagggcagc cccgagaacc acaggtgtac accctgcccc catcccggga ggagatgacc 420
 aagaaccagg tcagcctgac ctgcctgggtc aaaggcttct accccagcga catcgccgtg 480
 gagtggggaga gcaatgggca gccggagaac aactacaaga ccacacctcc catgctggac 540
 tccgacggct ccttcttctt ctacagcaag ctcaccgtgg acaagagcag gtggcagcag 600
 gggaaacgtct tctcatgctc cgtgatgcat gaggtctctgc acaaccacta cacacagaag 660
 agcctctccc tgtctccggg taaatga 687

<210> 39
 <211> 229
 <212> PRT
 <213> Homo Sapiens

<400> 39

Glu Ser Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe
 1 5 10 15

Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
 20 25 30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
 35 40 45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
50 55 60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65 70 75 80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
85 90 95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
100 105 110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
115 120 125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
130 135 140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145 150 155 160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
165 170 175

Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
180 185 190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
195 200 205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
210 215 220

Leu Ser Leu Gly Lys
225

<210> 40

<211> 690

<212> DNA

<213> HS

<400> 40

gagtcctaaat atggtccccc atgcccataca tgcccagcac ctgagttcct ggggggacca 60

tcagtcttcc tgttcccccc aaaacccaag gacactctca tgatctcccg gaccctgag 120

gtcacgtgcg tgggtggtgga cgtgagccag gaagaccccg aggtccagtt caactggtac 180

gtggatggcg tggaggtgca taatgccaag acaaagccgc gggaggagca gttcaacagc 240


```

acgtaccgtg tggtcagcgt cctcacgcgc ctgcaccagg actggctgar cggcaaggag      300
tacaagtgca aggtctccar caaaggcctc ccgtcctcca tcgagaaaac catctccaam      360
gccamagggc agccccgaga gccacaggtg tacaccctgc ccccatccca ggaggagatg      420
accaagaacc aggtcagcct gacctgcctg gtcaaaggct tctaccccag cgacatcgcc      480
gtggagtggg agagcaatgg gcagccggag aacaactaca agaccacgcc tcccgtgctg      540
gactccgacg gctccttctt cctctacagc aggctaaccg tggacaagag cagktggcag      600
gaggggaatg tcttctcatg ctccgtgatg catgaggctc tgcacaacca ctacacacag      660
aagagcctct ccctgtctct gggtaaatga                                     690

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<210> 41
 <211> 585
 <212> PRT
 <213> HS

<400> 41

```

Asp Ala His Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu
1              5              10              15

```

```

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
                20              25              30

```

```

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
          35              40              45

```

```

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
50              55              60

```

```

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65              70              75              80

```

```

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
          85              90              95

```

```

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
          100              105              110

```

```

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
          115              120              125

```

```

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
130              135              140

```

Arg His Pro Tyr Phe Tyr Ala Pro Gln Leu Leu Phe Phe Ala Lys Arg
 145 150 155 160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
 165 170 175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
 180 185 190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
 195 200 205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
 210 215 220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
 225 230 235 240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
 245 250 255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
 260 265 270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
 275 280 285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
 290 295 300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
 305 310 315 320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
 325 330 335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
 340 345 350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Pro Asp Pro His Glu
 355 360 365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Met Glu Glu Pro
 370 375 380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Gln Leu Gly Glu

385

390

395

400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
 405 410 415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
 420 425 430

Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
 435 440 445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
 450 455 460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
 465 470 475 480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
 485 490 495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
 500 505 510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
 515 520 525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
 530 535 540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
 545 550 555 560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
 565 570 575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
 580 585

<210> 42

<211> 1758

<212> DNA

<213> HS

<400> 42

gatgcacaca agagtgaggt tgctcatcgg tttaaagatt tgggagaaga aaatttcaaa 60

gccttggtgt tgattgcctt tgctcagtat cttcagcagt gtccatttga agatcatgta 120

```

aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa      180
aattgtgaca aatcacttca tacccttttt ggagacaaat tatgcacagt tgcaactctt      240
cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa      300
tgcttcttgc aacacaaaga tgacaatcca aatctccccc gattgggtgag accagagggt      360
gatgtgatgt gcaactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat      420
gaaattgcca gaagacatcc ttacttttat gccccgcaac tccttttctt tgctaaaagg      480
tataaagctg cttttacaga atggtgccaa gctgctgata aagcagcctg cctggtgcca      540
aagctcgatg aacttcggga tgaagggaag gcttcgtctg ccaaacagag actcaagtgt      600
gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc      660
cagagatttc ccaaagctga gtttgacaga gtttccaagt tagtgacaga tcttaccaaa      720
gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgacag ggcggacctt      780
gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa      840
aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct      900
gacttgccct cattagcggc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct      960
gaggcaaagg atgtcttctt gggcatgttt ttgtatgaat atgcaagaag gcacccctgat     1020
tactctgtcg tactgctgct gagacttgcc aagacatatg aaaccactct agagaagtgc     1080
tgtgccgctc cagatcctca tgaatgctat gccaaagtgt tcgatgaatt taaacctctt     1140
atggaagagc ctcaagaattt aatcaaacia aattgtgagc tttttgagca gcttgagag     1200
tacaaattcc agaatgcgct attagtctgt tacaccaaga aagtacccca agtgtcaact     1260
ccaactcttg tagaggtctc aagaaacctg ggaaaagtgg gcagcaaattg ttgtaaacat     1320
cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggctct gaaccagtta     1380
tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc     1440
ttggtgaaca ggcgaccatg cttttcagct ctggaagtgc atgaaacata cgttcccaaa     1500
gagtttaatg ctgaaacatt caccttccat gcagatatat gcacactttc tgagaaggag     1560
agacaaatca agaaacaaac tgcacttggt gagcttgtga aacacaagcc caaggcaaca     1620
aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag     1680
gctgacgata aggaaacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa     1740
gctgccttag gcttataa                                     1758

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<210> 43
 <211> 110
 <212> PRT
 <213> Homo Sapiens

<400> 43

Met Arg Phe Met Thr Leu Leu Phe Leu Thr Ala Leu Ala Gly Ala Leu
 1 5 10 15

Val Cys Ala Tyr Asp Pro Glu Ala Ala Ser Ala Pro Gly Ser Gly Asn
 20 25 30

Pro Cys His Glu Ala Ser Ala Ala Gln Lys Glu Asn Ala Gly Glu Asp
 35 40 45

Pro Gly Leu Ala Arg Gln Ala Pro Lys Pro Arg Lys Gln Arg Ser Ser
 50 55 60

Leu Leu Glu Lys Gly Leu Asp Gly Ala Lys Lys Ala Val Gly Gly Leu
 65 70 75 80

Gly Lys Leu Gly Lys Asp Ala Val Glu Asp Leu Glu Ser Val Gly Lys
 85 90 95

Gly Ala Val His Asp Val Lys Asp Val Leu Asp Ser Val Leu
 100 105 110

<210> 44

<211> 333

<212> DNA

<213> HS

<400> 44

atgagggttca tgactctcct cttcctgaca gctctggcag gagccctgggt ctgtgcctat 60
 gatccagagg ccgcctctgc cccaggatcg ggggaaccctt gccatgaagc atcagcagct 120
 caaaaggaaa atgcaggtga agaccaggg ttagccagac aggcaccaa gccaaaggaag 180
 cagagatcca gccttctgga aaaaggccta gacggagcaa aaaaagctgt ggggggactc 240
 ggaaaactag gaaaagatgc agtcgaagat ctagaaagcg tgggtaaagg agccgtccat 300
 gacgttaaag acgtccttga ctcagtacta tag 333

<210> 45

<211> 21

<212> DNA

<213> Artificial

<220>

<223> Synthesized Sequence

<400> 45

aacccttgcc atgaagcatc a

21

<210> 46
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 46
aagcatcagc agctcaaaag g 21

<210> 47
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 47
aaaaggaaaa tgcaggtgaa g 21

<210> 48
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 48
aaaggaaaat gcaggtgaag a 21

<210> 49
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 49
aaggaaaatg caggtgaaga c 21

<210> 50
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 50
aaaatgcagg tgaagaccca g 21

<210> 51
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized sequence

<400> 51
aaatgcaggt gaagacccag g 21

<210> 52
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 52
aaagccaagg aagcagagat c 21

<210> 53
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 53
aagccaagga agcagagatc c 21

<210> 54
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 54
aaggaagcag agatccagcc t 21

<210> 55
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 55
aagcagagat ccagccttct g 21

<210> 56

<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 56
aaaaaggcct agacggagca a 21

<210> 57
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized sequence

<400> 57
aaaaggccta gacggagcaa a 21

<210> 58
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 58
aaaggcctag acggagcaaa a 21

<210> 59
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 59
aaggcctaga cggagcaaaa a 21

<210> 60
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 60
aaactaggaa aagatgcagt c 21

<210> 61
<211> 21

<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 61
aactaggaaa agatgcagtc g 21

<210> 62
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 62
aaaagatgca gtcgaagatc t 21

<210> 63
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 63
aaagatgcag tcgaagatct a 21

<210> 64
<211> 21
<212> DNA
<213> Artificial

<220>
<223> Synthesized Sequence

<400> 64
aagatgcagt cgaagatcta g 21

<210> 65
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 Glu Thr Gln Phe Asn Gln Tyr Lys Thr Glu Ala Ala Ser Arg Tyr Asn
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